

SEQUENCE LISTING

<110> Cahoon, Edgar B.
Hitz, William D.
Kinney, Anthony J.
Vollmer, Steven J.

<120> LIMNANTHES OIL GENES

<130> BB1117 US NA

<140>
<141>

<150> 60/078,736
<151> 1998-03-20

<150> PCT/US99/05471
<151> 1999-03-12

<160> 7

<170> MICROSOFT OFFICE 97

<210> 1
<211> 1355
<212> DNA
<213> *Limnanthes douglasii*

<400> 1

gcttgagact ctctctctac ttccccatct ctatatctct ctctctctct ctagaagcca 60
tggcttcattt catcgcaacc acaacaccag caatgccagc tttcgcttca gttcttgatc 120
caaaaatacc cacaacccca gaacccaaaa cggaaacccc caaaccaaaa gacgatctcg 180
aacgcttccg gacatcagaa gtcgttgg agaggaaatc caaaggattc tggcgccgga 240
aatggAACCC tcgtatattt caaaaccccg tcacttact ggtcctgcat gcttttgatc 300
cgatggcgcc ctttatttc agctggatg cgtttggat ctctttatc ttgcttggatc 360
tcgcaagcgg tggcttggatc atcactttgt gctccatag gtgttactt catggcggtt 420
tcaagcttcc taagttggatc ggttacttctt tggcttactt tggcttcattt gctcttcagg 480
gagatcccat ggaatgggtt agcaaccata ggttccatca ccagttcgatc gatacagaaa 540
gagatgttca tagtccaaact caaggatttt gtttctgtca cattgggttgg gtttttgatc 600
aagattttt cgtcggaaaa cgtggggcc gaagaaacaa tgtaatgtatc ttgaagaaac 660
aaggcttcta cagatttcctc cagaaaaactt atatgtatca tcaattggct ctaatagctc 720
tacttttacta cgtcgaggg tttccatata ttgttctgggg aatgggtttt agattgggtt 780
ttatgttccca ttccatattt gctatcaact cagtttgcata taaatggggc ggaaggccat 840
ggaatactgg agattttatcg accaacaata ttttttttttgc atttttttttgc tttggagagg 900
gctggcataa caaccaccac gcatttgcac aatcgttgc acacgggtttaa gatggggc 960
agatcgatgt tactggatc gtttccatata ctcttccatata ttttttttttgc gtttccatata 1020
tgaagcttacc aactgaagct cagaagccaa agcttccatata aatgggtttttaa gatggggc 1080
gaagcatgttataatgttgcata ctttccatata ttttttttttgc gtttccatata 1140
tgtaatgttgcata aatgggttttgcata ctttccatata ttttttttttgc gtttccatata 1200
ttcttgcata ttttttttttgcata ctttccatata ttttttttttgc gtttccatata 1260
gcttgggttgcata ttttttttttgcata ctttccatata ttttttttttgc gtttccatata 1320
ttatatatatag ttttttttttgcata ctttccatata ttttttttttgc gtttccatata 1355

<210> 2

<211> 356

<212> PRT

<213> *Limnanthes douglasii*

<400> 2

Leu Arg Leu Ser Leu Tyr Phe Pro Ile Ser Ile Ser Leu Ser Leu Ser
1 5 10 15

Leu Glu Ala Met Ala Ser Phe Ile Ala Thr Thr Thr Pro Ala Met Pro
20 25 30

Ala Phe Ala Ser Val Leu Asp Pro Lys Ile Pro Thr Lys Pro Glu Pro
 35 40 45
 Lys Thr Glu Thr Pro Lys Pro Lys Asp Asp Leu Glu Arg Phe Arg Thr
 50 55 60
 Ser Glu Val Val Leu Glu Arg Lys Ser Lys Gly Phe Trp Arg Arg Lys
 65 70 75 80
 Trp Asn Pro Arg Asp Ile Gln Asn Ala Val Thr Leu Leu Val Leu His
 85 90 95
 Ala Leu Ala Ala Met Ala Pro Phe Tyr Phe Ser Trp Asp Ala Phe Trp
 100 105 110
 Ile Ser Phe Ile Leu Leu Gly Phe Ala Ser Gly Val Leu Gly Ile Thr
 115 120 125
 Leu Cys Phe His Arg Cys Leu Thr His Gly Gly Phe Lys Leu Pro Lys
 130 135 140
 Leu Val Glu Tyr Phe Phe Ala Tyr Cys Gly Ser Leu Ala Leu Gln Gly
 145 150 155 160
 Asp Pro Met Glu Trp Val Ser Asn His Arg Tyr His His Gln Phe Val
 165 170 175
 Asp Thr Glu Arg Asp Val His Ser Pro Thr Gln Gly Phe Trp Phe Cys
 180 185 190
 His Ile Gly Trp Val Leu Asp Lys Asp Leu Phe Val Glu Lys Arg Gly
 195 200 205
 Gly Arg Arg Asn Asn Val Asn Asp Leu Lys Lys Gln Ala Phe Tyr Arg
 210 215 220
 Phe Leu Gln Lys Thr Tyr Met Tyr His Gln Leu Ala Leu Ile Ala Leu
 225 230 235 240
 Leu Tyr Tyr Val Gly Gly Phe Pro Tyr Ile Val Trp Gly Met Gly Phe
 245 250 255
 Arg Leu Val Phe Met Phe His Ser Thr Phe Ala Ile Asn Ser Val Cys
 260 265 270
 His Lys Trp Gly Gly Arg Pro Trp Asn Thr Gly Asp Leu Ser Thr Asn
 275 280 285
 Asn Met Phe Val Ala Leu Cys Ala Phe Gly Glu Gly Trp His Asn Asn
 290 295 300
 His His Ala Phe Glu Gln Ser Ala Arg His Gly Leu Glu Trp Trp Gln
 305 310 315 320
 Ile Asp Val Thr Trp Tyr Val Ile Arg Thr Leu Gln Ala Ile Gly Leu
 325 330 335
 Ala Thr Asn Val Lys Leu Pro Thr Glu Ala Gln Lys Gln Lys Leu Lys
 340 345 350
 Ala Lys Ser Ala
 355

<210> 3
 <211> 305

<212> PRT
 <213> Arabidopsis thaliana
 <400> 3
 Met Ser Leu Ser Ala Ser Glu Lys Glu Glu Asn Asn Lys Lys Met Ala
 1 5 10 15
 Ala Asp Lys Ala Glu Met Gly Arg Lys Lys Arg Ala Met Trp Glu Arg
 20 25 30
 Lys Trp Lys Arg Leu Asp Ile Val Lys Ala Phe Ala Ser Leu Phe Val
 35 40 45
 His Phe Leu Cys Leu Leu Ala Pro Phe Asn Phe Thr Trp Pro Ala Leu
 50 55 60
 Arg Val Ala Leu Ile Val Tyr Thr Val Gly Gly Leu Gly Ile Thr Val
 65 70 75 80
 Ser Tyr His Arg Asn Leu Ala His Arg Ser Phe Lys Val Pro Lys Trp
 85 90 95
 Leu Glu Tyr Phe Phe Ala Tyr Cys Gly Leu Leu Ala Ile Gln Gly Asp
 100 105 110
 Pro Ile Asp Trp Val Ser Thr His Arg Tyr His His Gln Phe Thr Asp
 115 120 125
 Ser Asp Arg Asp Pro His Ser Pro Asn Glu Gly Phe Trp Phe Ser His
 130 135 140
 Leu Leu Trp Leu Phe Asp Thr Gly Tyr Leu Val Glu Lys Cys Gly Arg
 145 150 155 160
 Arg Thr Asn Val Glu Asp Leu Lys Arg Gln Trp Tyr Tyr Lys Phe Leu
 165 170 175
 Gln Arg Thr Val Leu Tyr His Ile Leu Thr Phe Gly Phe Leu Leu Tyr
 180 185 190
 Tyr Phe Gly Gly Leu Ser Phe Leu Thr Trp Gly Met Gly Ile Gly Val
 195 200 205
 Ala Met Glu His His Val Thr Cys Leu Ile Asn Ser Leu Cys His Val
 210 215 220
 Trp Gly Ser Arg Thr Trp Lys Thr Asn Asp Thr Ser Arg Asn Val Trp
 225 230 235 240
 Trp Leu Ser Val Phe Ser Phe Gly Glu Ser Trp His Asn Asn His His
 245 250 255
 Ala Phe Glu Ser Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp
 260 265 270
 Ile Ser Trp Tyr Ile Val Arg Phe Leu Glu Ile Ile Gly Leu Ala Thr
 275 280 285
 Asp Val Lys Leu Pro Ser Glu Ser Gln Arg Arg Arg Met Ala Met Val
 290 295 300
 Arg
 305
 <210> 4
 <211> 1807

006760-01049960

<212> DNA
<213> *Limnanthes douglasii*

<220>
<221> unsure
<222> (302)..(303)

<220>
<221> unsure
<222> (312)

<220>
<221> unsure
<222> (315)

<220>
<221> unsure
<222> (421)

<220>
<221> unsure
<222> (1727)

<400> 4

ctcaactctca	caccccttc	tctcttttgc	tcggcttc	cggcagata	ctcaacggat	60
tcaatcgaa	ggtagtacaa	tatgtcggag	acaaaacctg	agaaacctt	gatcgcaacc	120
gtgaaaaaca	cactaccta	tttaaaacta	tcaataaaact	taaaacacgt	gaaactcggt	180
taccattacc	tgatcaccca	tggaatgtac	ctgtgtctcc	ctccctctc	actagtccctc	240
ttcgctcaaa	tctcaacttt	gtccctcaaa	gatttcaacg	acatctggaa	acagcttcag	300
tnnaatctca	tntcngtcgt	tgtttcatca	acacttcttg	tctccttact	tatcctttac	360
ttcatgactc	gtccgaggcc	ggtttatttg	atggatttgc	cgtgtataa	acccgacgaa	420
nctcgaaaat	ctactagaga	acattttatg	aagtgtgggt	agagtttggg	ctctttacg	480
gaggataata	tcgattttca	gaggaaatta	gtcgacgat	ctggacttgg	tgatgctacg	540
tatttaccc	aagctatcg	tactatcccg	gctcatccgt	cgatgaaagc	tgcgagaaga	600
gaagctgagt	ttgtgtatgtt	ttgtgcgatt	gatcaactt	tggagaagac	aaaggtgaat	660
ccgaaggata	tagggatctt	ggttttaat	tgcagcctgt	ttagtcgcac	tccgtccctc	720
tcgtcgatga	ttgttaacca	ctataaaactc	cgtggaaaca	ttataagcta	caatctaggc	780
ggaatgggtt	gcagtgcgtt	tttaatttcg	gtcgacttag	ctaaaagact	tctcgagaca	840
aatccaaaca	cttacgctt	agttatgagc	actgaaaata	tcacactaaa	ctggtacatg	900
ggcaatgacc	ggtccaaact	cgtgtccaaat	tgtctttcc	ggatgggagg	agctgcggtc	960
ttgttatcaa	acaaaacctc	tgataagaaa	agatcgaagt	atcagtttgt	tactaccgtc	1020
cgaagccaca	aagggtctga	cgataattgc	tacgggtc	tatccaaga	agaagactcc	1080
aacggcaaaa	tcgggtgtaa	cctctccaaa	aatctaattgg	cggtcgcagg	ggacgcgctt	1140
aagactaaca	tcacgacgt	tggtcgttgc	gttttaccaa	tgtcggaaaca	acttttgc	1200
ttcgccacgc	tggttgctcg	aaaagtttca	aagaagaaaa	ttaagcccta	cattccggac	1260
tttaaacttag	cttttgatca	tttctgtatt	catgcgggttgc	gtcgagctgt	tttggacgag	1320
cttgagaaga	atttgcagtt	gtcaagctgg	catctagagc	cgtcgagaat	gacgtttatc	1380
cggtttggta	atacgtcgag	tagtacttttgc	tggtacgagc	tggcgtattc	ggaagccaaa	1440
gggaggat	gaaaaggaga	aagagtttgc	cagataggtt	ttggttctgg	gtttaaatgt	1500
aatagtgtc	tctggaaagc	cttaaagagc	gttgcatttca	agaaagagaa	caatccatgg	1560
atggatgaga	tccaccagtt	tccgggttgc	gttgcataag	gttgcgttttgc	gatgttaat	1620
gtttgggtgt	ttgtatgcttgc	ctaattgggtt	agtgtaaagaa	gtacttgggtt	gtcgctgttt	1680
caattactaa	ctaaagagag	tgttgaataa	gcatagaaca	aagtaantaa	ctggaaagtgc	1740
cttigttgtt	tgttgcgtt	ctctattact	gttgcatttgc	tctcaagagaa	agaattatgt	1800
ttaaaaaa						1807

006760-006760

<220>
<221> UNSURE
<222> (77)

<220>
<221> UNSURE
<222> (114)

<400> 5
Met Ser Glu Thr Lys Pro Glu Lys Pro Leu Ile Ala Thr Val Lys Asn
1 5 10 15
Thr Leu Pro Asp Leu Lys Leu Ser Ile Asn Leu Lys His Val Lys Leu
20 25 30
Gly Tyr His Tyr Leu Ile Thr His Gly Met Tyr Leu Cys Leu Pro Pro
35 40 45
Leu Ala Leu Val Leu Phe Ala Gln Ile Ser Thr Leu Ser Leu Lys Asp
50 55 60
Phe Asn Asp Ile Trp Glu Gln Leu Gln Xaa Asn Leu Xaa Ser Val Val
65 70 75 80
Val Ser Ser Thr Leu Leu Val Ser Leu Leu Ile Leu Tyr Phe Met Thr
85 90 95
Arg Pro Arg Pro Val Tyr Leu Met Asp Phe Ala Cys Tyr Lys Pro Asp
100 105 110
Glu Xaa Arg Lys Ser Thr Arg Glu His Phe Met Lys Cys Gly Glu Ser
115 120 125
Leu Gly Ser Phe Thr Glu Asp Asn Ile Asp Phe Gln Arg Lys Leu Val
130 135 140
Ala Arg Ser Gly Leu Gly Asp Ala Thr Tyr Leu Pro Glu Ala Ile Gly
145 150 155 160
Thr Ile Pro Ala His Pro Ser Met Lys Ala Ala Arg Arg Glu Ala Glu
165 170 175
Leu Val Met Phe Gly Ala Ile Asp Gln Leu Leu Glu Lys Thr Lys Val
180 185 190
Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Ser
195 200 205
Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His Tyr Lys Leu Arg
210 215 220
Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
225 230 235 240
Leu Ile Ser Val Asp Leu Ala Lys Arg Leu Leu Glu Thr Asn Pro Asn
245 250 255
Thr Tyr Ala Leu Val Met Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr
260 265 270
Met Gly Asn Asp Arg Ser Lys Leu Val Ser Asn Cys Leu Phe Arg Met
275 280 285
Gly Gly Ala Ala Val Leu Leu Ser Asn Lys Thr Ser Asp Lys Lys Arg
290 295 300

D06T60-D07T60

Ser Lys Tyr Gln Leu Val Thr Thr Val Arg Ser His Lys Gly Ala Asp
305 310 315 320

Asp Asn Cys Tyr Gly Cys Ile Phe Gln Glu Glu Asp Ser Asn Gly Lys
325 330 335

Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala Val Ala Gly Asp Ala
340 345 350

Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser
355 360 365

Glu Gln Leu Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys
370 375 380

Lys Lys Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Asp His
385 390 395 400

Phe Cys Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Leu Glu Lys
405 410 415

Asn Leu Gln Leu Ser Ser Trp His Leu Glu Pro Ser Arg Met Thr Phe
420 425 430

Ile Arg Phe Gly Asn Thr Ser Ser Ser Thr Leu Trp Tyr Glu Leu Ala
435 440 445

Tyr Ser Glu Ala Lys Gly Arg Ile Arg Lys Gly Glu Arg Val Trp Gln
450 455 460

Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala
465 470 475 480

Leu Lys Ser Val Asp Pro Lys Lys Glu Asn Asn Pro Trp Met Asp Glu
485 490 495

Ile His Gln Phe Pro Val Ala Val Val
500 505

<210> 6

<211> 844

<212> DNA

<213> *Limnanthes douglasii*

<400> 6

acacggggcaa tgaccgatcg aaactcgtgt ctaattgtct tttccgtatg ggaggagctg 60
cggtttatt atcaaacaaa cattcgaca aaaaacgatc gaaataccag ttggttacta 120
ccgtccgaag ccacaaaagggt gctgacgata attgctatgg ctgcacatctt caagaagagg 180
actcgactgg aataagtggt gtaagtctct cgaaaaatct aatggcagtc gcaggcgatg 240
cactcaagac aaacatcacg acgatcggtc cgtagtttt accaatgact gaacaacttt 300
tgtattttgc ctccctggtc ggccgaaata ttttcaaaaat gaaaataaaaa acctacgttc 360
ccgattttaa actcgccttc gaggattctt gtattcacgc aggtggtcga ggagtgttgg 420
acgcgcgttga gaagaatttg cagttgtcgg agtggcatct tgagccatcg aggatgacgt 480
tgtaccgatt tggtaatacgt tcgagtagta gtttatggta tgagctggcg tattcggaaag 540
ccaaaggggag aattaagaag ggagagaggg tttggcagat agggtttggt tcagggttta 600
agtgtaatag tgggtttgg aaagcgctac ggacagtaga tccgaaggaa gagaataatc 660
cttggacgga tgagatccac cagtttccag ttgctgttgt ctgagtttat gttggatgtt 720
tgaagtaaac ttaatgtttt ggtctgggtgt ccatgctgag attagtgcag caactcttt 780
gcgaaataat aaatgcttag aaactgtttt gttgtttaaa aaaaaaaaaa aaaaaaaaaa 840
aaaa 844

<210> 7

<211> 233

<212> PRT

<213> *Limnanthes douglasii*

<400> 7
 Thr Gly Asn Asp Arg Ser Lys Leu Val Ser Asn Cys Leu Phe Arg Met
 1 5 10 15
 Gly Gly Ala Ala Val Leu Leu Ser Asn Lys His Ser Asp Lys Lys Arg
 20 25 30
 Ser Lys Tyr Gln Leu Val Thr Thr Val Arg Ser His Lys Gly Ala Asp
 35 40 45
 Asp Asn Cys Tyr Gly Cys Ile Phe Gln Glu Glu Asp Ser Thr Gly Ile
 50 55 60
 Ser Gly Val Ser Leu Ser Lys Asn Leu Met Ala Val Ala Gly Asp Ala
 65 70 75 80
 Leu Lys Thr Asn Ile Thr Thr Ile Gly Pro Leu Val Leu Pro Met Thr
 85 90 95
 Glu Gln Leu Leu Tyr Phe Ala Ser Leu Val Gly Arg Asn Ile Phe Lys
 100 105 110
 Met Lys Ile Lys Thr Tyr Val Pro Asp Phe Lys Leu Ala Phe Glu His
 115 120 125
 Phe Cys Ile His Ala Gly Gly Arg Gly Val Leu Asp Ala Leu Glu Lys
 130 135 140
 Asn Leu Gln Leu Ser Glu Trp His Leu Glu Pro Ser Arg Met Thr Leu
 145 150 155 160
 Tyr Arg Phe Gly Asn Thr Ser Ser Ser Leu Trp Tyr Glu Leu Ala
 165 170 175
 Tyr Ser Glu Ala Lys Gly Arg Ile Lys Lys Gly Glu Arg Val Trp Gln
 180 185 190
 Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala
 195 200 205
 Leu Arg Thr Val Asp Pro Lys Glu Glu Asn Asn Pro Trp Thr Asp Glu
 210 215 220
 Ile His Gln Phe Pro Val Ala Val Val
 225 230